

Figure 1



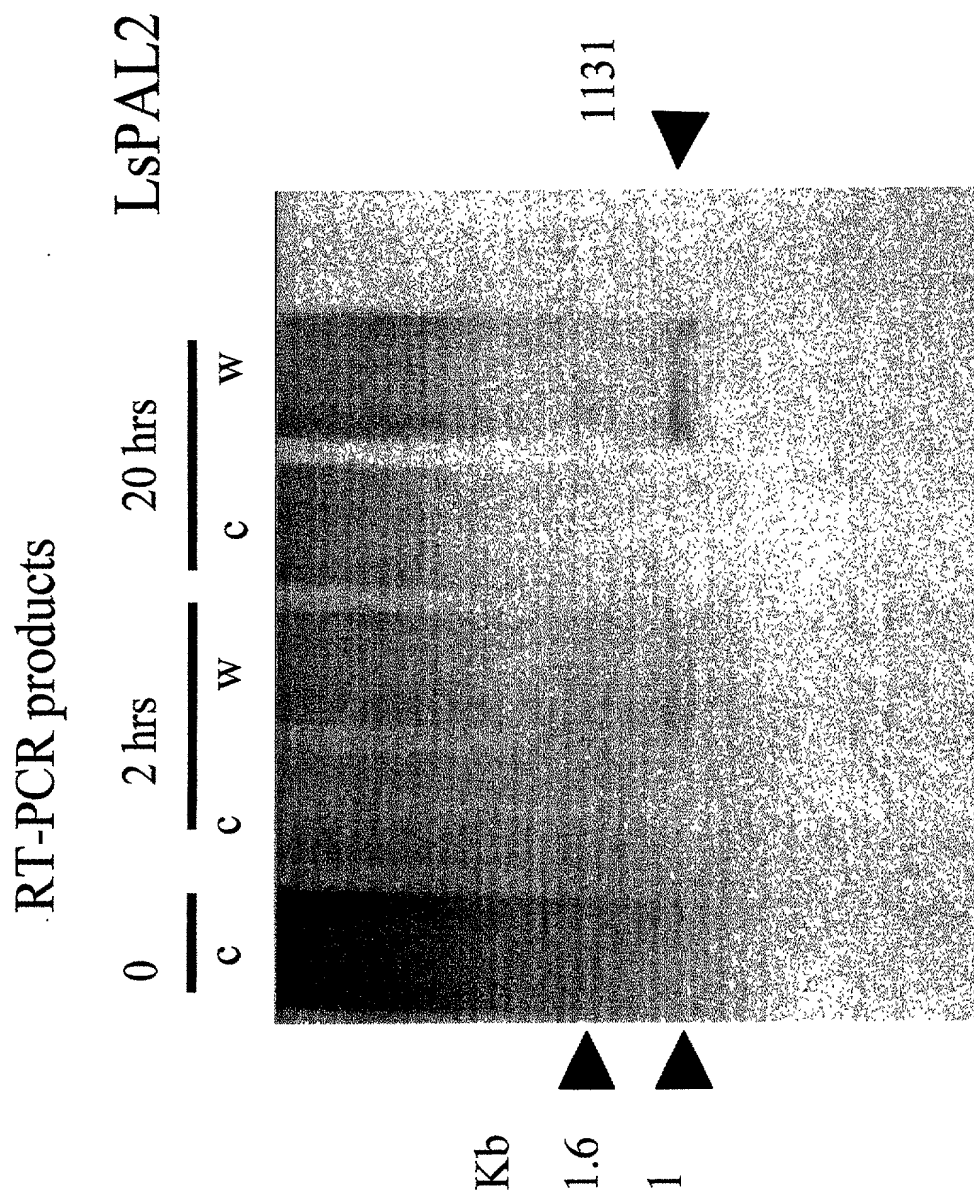


Figure 3

# Domains

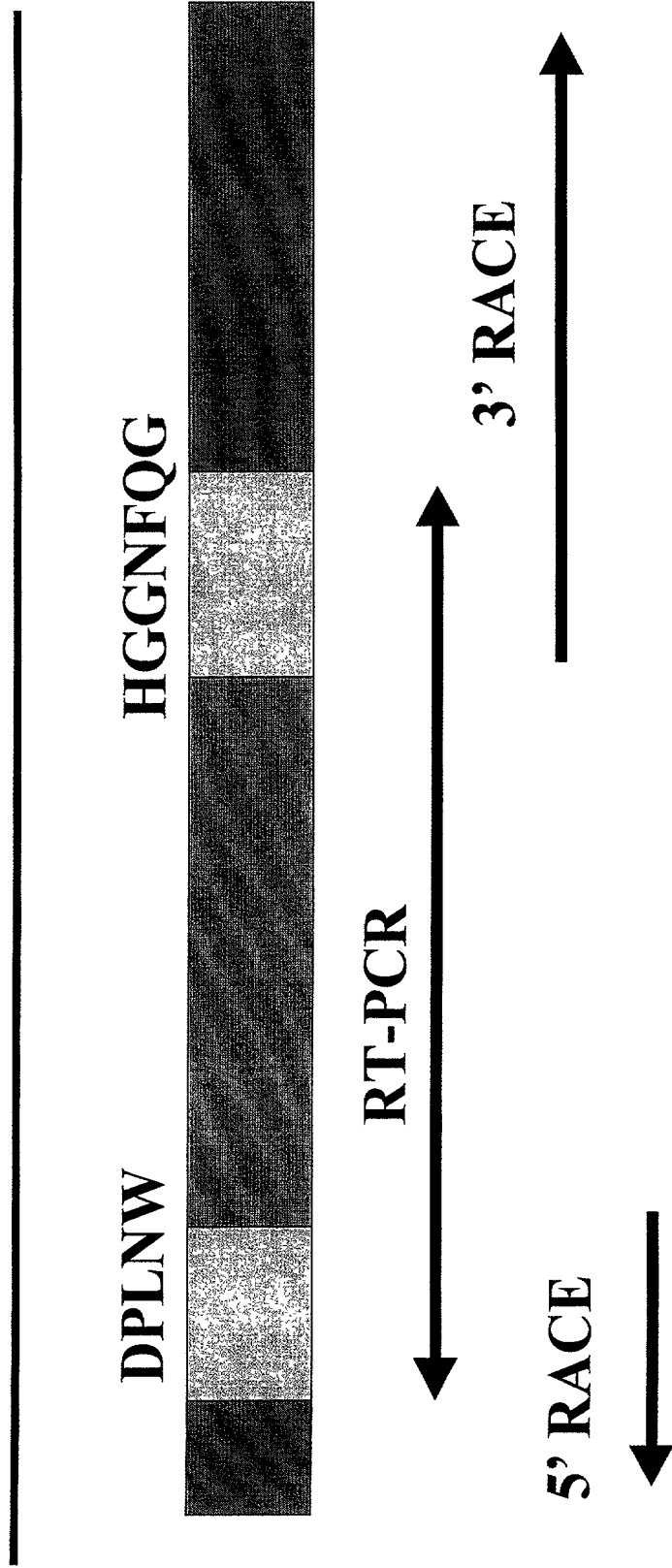


Figure 4

# PAL1

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1 GAGCAATCTG ATCAATACCC ATTCACGCAC AAAGAGTGTG AGTCTAGTGT GTGAAGAAGT
61 ACACAATTAG ATTGTTCTTG TTTCTTTGAT CTATAGTCTA CAATCTGTAT AAATAATAAT
121 GGAGAACGGT AATCACGTTA ATGGAGTCGT TAATGAGTTG TGCATCAAGG ATCCATTGAA
181 CTGGGGAGTT GCAGCGGAGG CGTTGACCGG AAGTCACCTT GATGAGGTGA AGAAGATGGT
241 TGCGGAGTTC AGAAAGCCGG TGGTGAAGCT CGGAGGAGAG ACGCTTACAG TTTCTCAGGT
301 GGCGGGGATC GCAGCTGCTA ATGACAGTGA CACCGTGAAG GTGGAGCTGT CGGAAGCCGC
361 GAGGGCTGGA GTTAAGGCGA GTAGTGATTG GGTATGGAG AGCATGAATA AAGGAACTGA
421 TAGTTATGGT GTCACCACCG GCTTCGGCGC CACCTCTCAC CGGAGAACTA AGCAAGGCGG
481 TGCTTTACAG AAGGAGCTCA TTAGATTTTT GAACGCCGGA ATATTCGGCA ATGGAACGGA
541 AACAAAGCCAC ACACTTCCAC ATTCAGCCAC CAGAGCCGCC ATGATCGTCA GAATCAACAC
601 CCTCCTCCAG GGTTACTCCG GCATCCGATT CGAGATCTTG GAAGCCATCA CCAAGTTCCT
661 TAACAACAAC ATCACCCTT GTTTACCCTT CCGTGGAACC ATCACCCTT CCGGTGACCT
721 TGTCCCATTA TCATACATCG CCGGCTCTT AACCGGCCGC CCCAACTCCA AAGCCGTTGG
781 CCCCACCGGA GAAGTCCTCA ATGCCGAAAA GGCCTTCGCT GCAGCCGGAG TTGAAGGTGG
841 GTTCTTCGAG TTACAGCCGA AAGAAGGGCT AGCACTTGTT AACGGCACCG CCGTGGGGTC
901 CGGGATGGCT TCCATGGTTC TATTTGATGC TAATGTACTT GCGTTGTTGT CGGAAGTGTT
961 ATCGGCGATC TTCGCTGAGG TTATGCAAGG GAAGCCGGAG TTTACCGATC ACTTGACACA
1021 CAAATTGAAG CATCACCTTG GTCAAATCGA GCGGCGGGCG ATCATGGAGT ATATTTTGGA
1081 CGGAAGCGAT TACGTCAAGG CGGCGCAAAA GGTCCACGAA ATGGACCCGT TACAGAAACC
1141 AAAACAAGAT CGTTATGCTC TCCGTACATC TCCCAATGG CTCGGACCTC AAATCGAAGT
1201 AATCCGATCA TCAACCAAAA TGATCGAGAG GGAAATCAAT TCCGTCAACG ACAACCCATT
1261 GATCGACGTT TCCAGAAACA AAGCTTTACA CCGTGGTAAC TTCCAAGGAA CCCCAATCGG
1321 AGTTTCCATG GACAACACCC GTCTCGCCAT TGCTGCAATC GGAAAACTCA TGTTTCGCTCA
1381 ATTTTCTGAG CTGGTTAACG ATTTCTACAA CAATGGATTA CCATCGAATC TCTCCGGTGG
1441 ACGTAACCCT AGTTTGGACT ACGGGTTCAA AGGTGGAGAA ATCGCCATGG CTCTTACTG
1501 TTCTGAGCTT CAGTTTCTCG CAAATCCAGT CACCAACCAT GTTCAAAGCG CCGAACAACA
1561 CAATCAAGAC GTTAATTCTC TCGGATTAAT TTCAGCGAGG AAAACCGCAG AAGCAGTCGA
1621 CATCTTAAAA CTCATGTCGT CGACATACTT AGTCGCTCTA TGCCAATCCA TCGATTTACG
1681 CCATTTGGAA GAGAACATGA AATCGACAGT GAAGAACACC GTAAGCCAAG TCGCGAAAAA
1741 GGTCTCACC ATGGGCGTCA ACGGCGAGCT CCACCCGTCG AGATTCTGCG AGAAAGATCT
1801 CCTCCGTGTT GTTGATCGTG AATACGTCTT CGCTTACATC GACGACGTTT GCAGCGGCAC
1861 ATACCCATTA ATGCAGAAGC TCCGACAGGT TCTGGTCGAC CACGCTCTAA ACAACGGCGA
1921 AACGGAGAAG AACACTAACA CCTCCATCTT CCAAAAAGATC GCTACCTTCG AAGAAGAATT
1981 GAAAGTCCTG TTACCGAAAAG AAGTTGAAGG TGTTAGAATC GCTTATGAGA ATGATACATT
2041 GTCGATTCCA AACAGGATTA AAGCTTGCAG ATCGTACCCG TTGTATAGGT TTGTAAGGGA
2101 GGAGCTCGGC AGAGGGTTTT TGACCGGAGA AAAGGTGACG TCGCCGGGAG AGGAGTTCGA
2161 CAGGGTGTTT ACGGCGATGT GCAAAGGTCA AATTATTGAT CCGTTGTTGG AGTGTCTTGG
2221 AGGGTGGAAT GGGGAACCTC TTCCAATATG TTAGGAAAGT GAGTGTGAAA CCGTTTGAAT
2281 TGTATTTGTA ATATTCTGTT TTTTCTTTT TTTTCTTAA TTTATTTGCA TTTAATATCT
2341 CATCAAAGAC TTCCACTTTC AAGTGTGGTG TATGTGGTTG TAAATCATAT ATATTAACCT
2401 ATTATTTTGG CTAAAAA AAAA AAAAAA AA

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Figure 5

Sequence I.D. No. 3

## PAL1

translation="MENGNHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVV  
KLGGETLTVSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGV  
TGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGY  
SGIRFEILEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLN  
AEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFA  
EVMQKGKPEFTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQD  
RYALRTSPQWLGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSM  
DNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSE  
LQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRH  
LEENMKSTVKNTVSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSG  
TYPLMQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYEND  
TLSIPNRIKACRSYPLYRFVREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL  
GGWNGEPLPIC"

Figure 6

Sequence I.D. No. 1

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Sequence I.D. No. 4

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## PAL2

MGSTEMEVD SHQNGERA EFCVKG DPLNWGMAAESLKGS HLDE  
VKRMVAEFRKPVVRLGGETLTVSQVAAIAASDNAGVKVELSET  
ARAGVKASSDWVMESMNKGTDSYGVT TGFGATSHRRTKEGGA  
LQKELIRFLNAGIFGNGTESTHTLPHSATRAAMLVRINTLLQGY  
SGIRFEILEAITKFLNHNVT PFLPLRGTITASGDLVPLSYIAGLLT  
GRANSKAVGPTGEVLNAEKAF AEAGVEGGFFELQPKEGLALV  
NGTAVGSGMASMVLF DANVLALLSEVL SAIFAEVMQ GKPEFTD  
HLTHKLKHHPGQIEAAAIM EYILDGSDYV KAAQKVHEMDPLQ  
KPKQDRYALRTSPQWLGPQIEVIRSSTKMIEREINSVNDNPLID  
VSRNKALHGGNFQGTPIGV SMDNTRLAIAAIGKLMFAQFSELV  
NDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLAN  
PVTNHVQSAEQHNQDVNSLGLISARKTAESVEILKLMSTTYLV  
ALCQSIDLRHLEENLKSTVKNTVSLVAKKILTTGVNGELHPSRF  
CEKDLLRVVDREYVFAYIDDACSATYPLMQKLRQVIVDHALN  
NENDAGTSIFQKISEFEEELKAVLPKEVEGVRSAYESSTLTIPNR  
IKECRSYPLYRFVREELGTGFLTGEEVTSPGEEFDKVFTALCKG  
HIIDPLLEC VQGWNGVPLPIS

Figure 8  
Sequence I.D. No. 2

+



1	MENGT	HVNGS	ANG	FC	IKDP	LNW	GVAA	EAL	TGSH	LD	EVKK	MVGE	FRK	PVVK	Sunflower		
1	MENGN	HVNGV	NVE	FC	IKDP	LNW	GVAA	EAL	TGSH	LD	EVKK	MVGE	FRK	PVVK	Lettuce		
51	LGGET	LT	VS	OVAG	IS	SAAG	DGNM	VK	VEL	SE	AR	AGV	KAS	SD	WM	Sunflower	
51	LGGET	LT	VS	OVAG	IAA	AN	DS	DT	VK	VEL	SE	AR	AGV	KAS	SD	WM	Sunflower
101	DSYGV	TG	FGAT	SH	RRTK	NG	GAL	OKEL	IRE	LN	AG	IE	GN	GTE	SSH	TP	PHSA
101	DSYGV	TG	FGAT	SH	RRTK	REG	GAL	OKEL	IRE	LN	AG	IE	GN	GTE	SSH	TP	PHSA
151	TRAAM	IV	RINT	LL	OGYS	GIR	FE	ILE	AIT	KFL	NNN	TP	CL	P	IR	GT	ITASGD
151	TRAAM	IV	RINT	LL	OGYS	GIR	FE	ILE	AIT	KFL	NNN	TP	CL	P	IR	GT	ITASGD
201	LVPLS	YI	AG	LL	TGR	P	NS	KAV	GP	A	GE	VL	NAE	S	A	F	AO
201	LVPLS	YI	AG	LL	TGR	P	NS	KAV	GP	A	GE	VL	NAE	S	A	F	AO
251	LALVNG	TAV	GSG	MA	SMV	L	FE	AN	V	L	A	L	S	E	V	L	S
251	LALVNG	TAV	GSG	MA	SMV	L	FE	AN	V	L	A	L	S	E	V	L	S
301	HKLKH	HP	G	O	I	E	A	A	I	M	E	Y	I	D	G	S	D
301	HKLKH	HP	G	O	I	E	A	A	I	M	E	Y	I	D	G	S	D
351	SPOM	L	G	P	O	I	E	V	I	R	S	A	T	K	M	I	E
351	SPOM	L	G	P	O	I	E	V	I	R	S	A	T	K	M	I	E
401	GVSMD	N	T	R	L	A	I	A	I	G	K	V	T	A	O	F	S
401	GVSMD	N	T	R	L	A	I	A	I	G	K	V	T	A	O	F	S
451	KGGE	I	A	M	A	S	Y	C	S	E	L	O	F	L	A	N	P
451	KGGE	I	A	M	A	S	Y	C	S	E	L	O	F	L	A	N	P
501	DILK	M	S	S	T	Y	L	V	A	L	C	O	S	I	D	L	R
501	DILK	M	S	S	T	Y	L	V	A	L	C	O	S	I	D	L	R
551	LHPS	R	F	C	E	K	D	L	R	V	D	R	E	V	E	F	A
551	LHPS	R	F	C	E	K	D	L	R	V	D	R	E	V	E	F	A
601	E	T	E	K	N	A	N	T	S	I	F	O	K	I	A	T	E
601	E	T	E	K	N	A	N	T	S	I	F	O	K	I	A	T	E
651	RSY	P	L	Y	R	E	V	R	E	L	G	G	A	-----	-----	-----	-----
651	RSY	P	L	Y	R	E	V	R	E	L	G	G	A	-----	-----	-----	-----
667	CGM	N	G	E	P	I	P	T	C	-----	-----	-----	-----	-----	-----	-----	-----
701	CGM	N	G	E	P	I	P	T	C	-----	-----	-----	-----	-----	-----	-----	-----

Figure 9

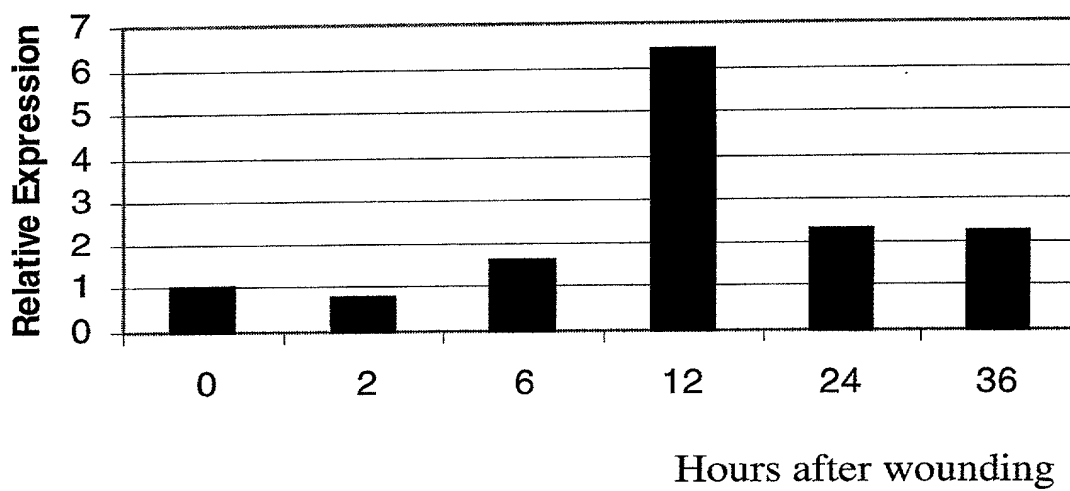
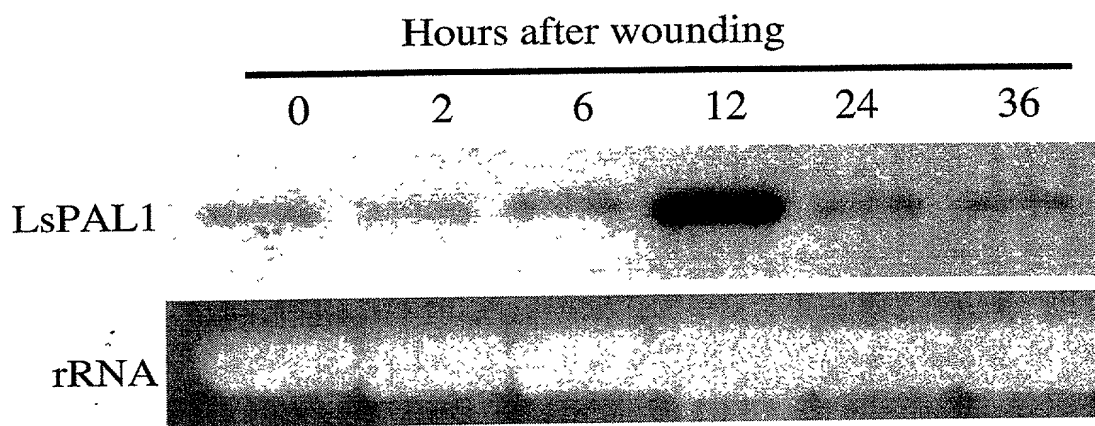


Figure 10

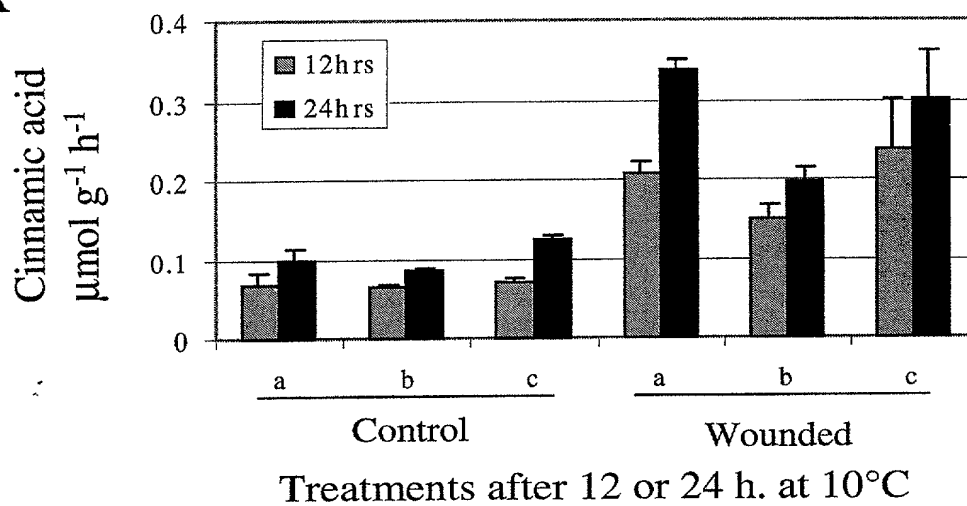
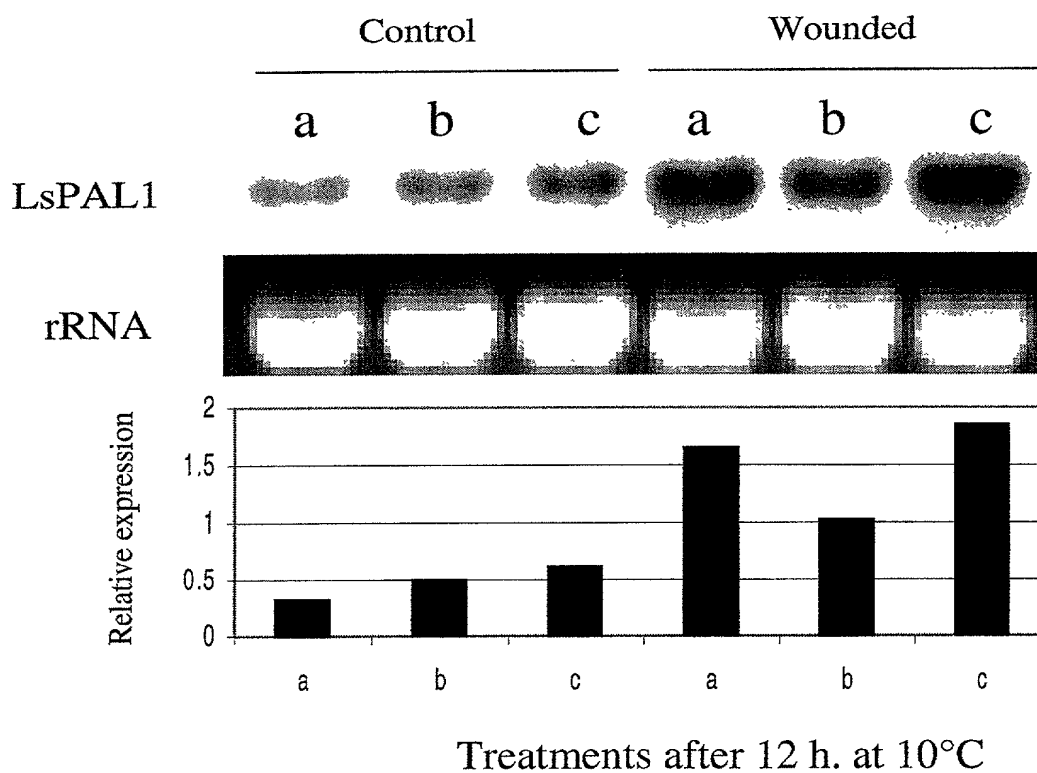
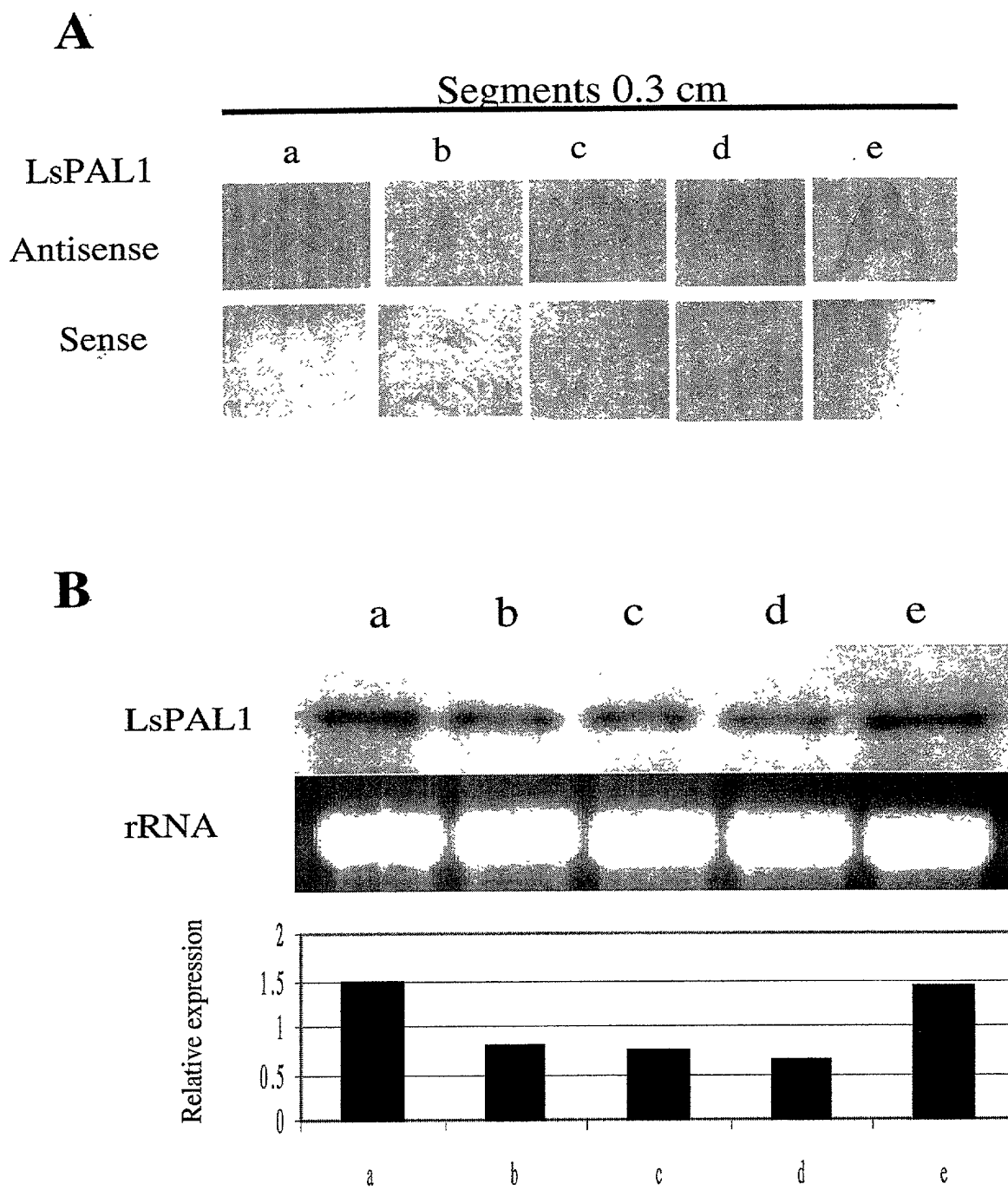
**A****B**

Figure 11



Northern from pieces in A

Figure 12